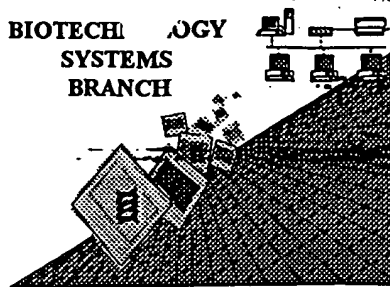


101A
1643

RAW SEQUENCE LISTING
ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



P#12
RECEIVED

OCT 05 2000

TECH CENTER 1600/2900

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/486,167

Source: 1643

Date Processed by STIC: 10-03-00

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

N/A

1643

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/486,167

DATE: 10/03/2000
TIME: 22:46:46

INPUT SET: S35961. RECEIVED

This Raw Listing contains the General
Information Section and up to the first 5 pages.

05/05/2000

TECH CENTER 1600/2900

Does Not Comply
Corrected Diskette Needed

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT:

~~(A) NAME: UNIVERSITE CATHOLIQUE DE LOUVAIN~~
Halles Universitaires
~~(B) STREET: Place de l'Universite, 1~~
~~(C) CITY: LOUVAIN LA-NEUVE~~
~~(E) COUNTRY: BELGIUM~~
~~(F) POSTAL CODE (ZIP): B-1348~~

(A) NAME: UNIVERSITE DE MONS-HAINAUT
(B) STREET: Place du Parc 20
(C) CITY: MONS
(E) COUNTRY: BELGIUM
(F) POSTAL CODE (ZIP): B-7000

(1) GENERAL INFORMATION:
(1) APPLICANT:
(2) TITLE OF INVENTION:
(3) NUMBER OF SEQUENCES:
(4) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE:
(B) STREET:
(C) CITY:
(D) STATE:
(E) COUNTRY:
(F) ZIP:

(ii) TITLE OF INVENTION: PEROXISOME-ASSOCIATED PEPTIDE, NUCLEOTIDE
SEQUENCE ENCODING SAID PEPTIDE AND THEIR USES IN THE
DIAGNOSTIC AND/OR THE TREATMENT OF LUNG INJURIES AND
DISEASES, AND OF OXIDATIVE STRESS-RELATED DISORDERS

(iii) NUMBER OF SEQUENCES: 19

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(4) COMPUTER READABLE FORM:
(A) MEDIUM TYPE:
(B) COMPUTER:
(C) OPERATING SYSTEM:
(D) SOFTWARE:
(5) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 805 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

EPO format
invalid for
U.S. applications.

RAW SEQUENCE LISTING PATENT APPLICATION US/09/486,167

DATE: 10/03/2000
TIME: 22:46:46

INPUT SET: S35961.raw

47 (vi) ORIGINAL SOURCE:
48 (A) ORGANISM: Homo sapiens
49
50 (ix) FEATURE:
51 (A) NAME/KEY: CDS
52 (B) LOCATION:193..681
53
54
55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
56
57 GCCAGGAGGC GGAGTGAAG TGGCCGTGGG GCGGGTATGG GACTAGCTGG CGTGTGCGG 60
58 CTGAGACGCT CAGCGGGCTA TATACTCGTC GGTGGGGCCG GCGGTCAGTC TGCGGCAGCG 120
59 GCAGCAAGAC GGTGCAGTGA AGGAGAGTGG GCGTCTGGCG GGGTCCGCAG TTTCAGCAGA 180
60
61 GCCGCTGCAG CC ATG GCC CCA ATC AAG GTG GGA GAT GCC ATC CCA GCA 228
62 Met Ala Pro Ile Lys Val Gly Asp Ala Ile Pro Ala
63 1 5 10
64
65 GTG GAG GTG TTT GAA GGG GAG CCA GGG AAC AAG GTG AAC CTG GCA GAG 276
66 Val Glu Val Phe Glu Gly Glu Pro Gly Asn Lys Val Asn Leu Ala Glu
67 15 20 25
68
69 CTG TTC AAG GGC AAG AAG GGT GTG CTG TTT GGA GTT CCT GGG GCC TTC 324
70 Leu Phe Lys Gly Lys Lys Gly Val Leu Phe Gly Val Pro Gly Ala Phe
71 30 35 40
72
73 ACC CCT GGA TGT TCC AAG ACA CAC CTG CCA GGG TTT GTG GAG CAG GCT 372
74 Thr Pro Gly Cys Ser Lys Thr His Leu Pro Gly Phe Val Glu Gln Ala
75 45 50 55 60
76
77 GAG GCT CTG AAG GCC AAG GGA GTC CAG GTG GTG GCC TGT CTG AGT GTT 420
78 Glu Ala Leu Lys Ala Lys Gly Val Gln Val Val Ala Cys Leu Ser Val
79 65 70 75
80
81 AAT GAT GCC TTT GTG ACT GGC GAG TGG GGC CGA GCC CAC AAG GCG GAA 468
82 Asn Asp Ala Phe Val Thr Gly Glu Trp Gly Arg Ala His Lys Ala Glu
83 80 85 90
84
85 GGC AAG GTT CGG CTC CTG GCT GAT CCC ACT GGG GCC TTT GGG AAG GAG 516
86 Gly Lys Val Arg Leu Leu Ala Asp Pro Thr Gly Ala Phe Gly Lys Glu
87 95 100 105
88
89 ACA GAC TTA TTA CTA GAT GAT TCG CTG GTG TCC ATC TTT GGG AAT CGA 564
90 Thr Asp Leu Leu Leu Asp Asp Ser Leu Val Ser Ile Phe Gly Asn Arg
91 110 115 120
92
93 CGT CTC AAG AGG TTC TCC ATG GTG GTA CAG GAT GGC ATA GTG AAG GCC 612
94 Arg Leu Lys Arg Phe Ser Met Val Val Gln Asp Gly Ile Val Lys Ala
95 125 130 135 140
96
97 CTG AAT GTG GAA CCA GAT GGC ACA GGC CTC ACC TGC AGC CTG GCA CCC 660
98
99

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OCT 05 2000

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RAW SEQUENCE LISTING PATENT APPLICATION US/09/486,167

DATE: 10/03/2000
TIME: 22:46:47

INPUT SET: S35961.raw

```

100 Leu Asn Val Glu Pro Asp Gly Thr Gly Leu Thr Cys Ser Leu Ala Pro
101           145                      150                      155
102
103 AAT ATC ATC TCA CAG CTC TGA GGCCCTGGGC CAGATTACTT CCTCCACCCC      711
104 Asn Ile Ile Ser Gln Leu *
105           160
106
107 TCCCTATCTC ACCTGCCCAG CCCTGTGCTG GGGCCCTGCA ATTGGAATGT TGGCCAGATT      771
108
109 TCTGCAATAA ACACTTGTGG TTTGCGGAAA AAAA      805
110
111
112 (2) INFORMATION FOR SEQ ID NO: 2:
113
114     (i) SEQUENCE CHARACTERISTICS:
115         (A) LENGTH: 162 amino acids
116         (B) TYPE: amino acid
117         (D) TOPOLOGY: linear
118
119     (ii) MOLECULE TYPE: protein
120     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
121
122 Met Ala Pro Ile Lys Val Gly Asp Ala Ile Pro Ala Val Glu Val Phe
123   1           5                      10                      15
124
125 Glu Gly Glu Pro Gly Asn Lys Val Asn Leu Ala Glu Leu Phe Lys Gly
126           20                      25                      30
127
128 Lys Lys Gly Val Leu Phe Gly Val Pro Gly Ala Phe Thr Pro Gly Cys
129           35                      40                      45
130
131 Ser Lys Thr His Leu Pro Gly Phe Val Glu Gln Ala Glu Ala Leu Lys
132           50                      55                      60
133
134 Ala Lys Gly Val Gln Val Val Ala Cys Leu Ser Val Asn Asp Ala Phe
135           65                      70                      75                      80
136
137 Val Thr Gly Glu Trp Gly Arg Ala His Lys Ala Glu Gly Lys Val Arg
138           85                      90                      95
139
140 Leu Leu Ala Asp Pro Thr Gly Ala Phe Gly Lys Glu Thr Asp Leu Leu
141           100                     105                     110
142
143 Leu Asp Asp Ser Leu Val Ser Ile Phe Gly Asn Arg Arg Leu Lys Arg
144           115                     120                     125
145
146 Phe Ser Met Val Val Gln Asp Gly Ile Val Lys Ala Leu Asn Val Glu
147           130                     135                     140
148
149 Pro Asp Gly Thr Gly Leu Thr Cys Ser Leu Ala Pro Asn Ile Ile Ser
150           145                     150                     155                     160
151
152 Gln Leu

```

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/486,167DATE: 10/03/2000
TIME: 22:46:47

INPUT SET: S35961.raw

153
154
155 (2) INFORMATION FOR SEQ ID NO: 3:
156
157 (i) SEQUENCE CHARACTERISTICS:
158 (A) LENGTH: 779 amino acids
159 (B) TYPE: nucleic acid
160 (C) STRANDEDNESS: single
161 (D) TOPOLOGY: linear
162
163 (ii) MOLECULE TYPE: DNA (genomic)
164
165 (iii) HYPOTHETICAL: NO
166
167 (iv) ANTI-SENSE: NO
168
169 (vi) ORIGINAL SOURCE:
170 (A) ORGANISM: Rattus Rattus
171
172 (ix) FEATURE:
173 (A) NAME/KEY: CDS
174 (B) LOCATION:136..624
175
176
177 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
178
179 TCGTCCTAG GCAGCATAGC CGGATCGGTG CTCCGTGCAT CGGCTACTTG GACGTGCGTG 60
180
181 GCAGGCAGAG CAGGCCGGA AGGAGCAGGT TGGGAGTGTG GTGGGGCCCG CAGCTTCAGC 120
182
183 AGTGCCGCGG TGA CTATGGC CCCGATCAAG GTGGGAGACA CCATTCCCTC AGTGGAGGTA 180
184
185 TTTGRAGGGG AACCTGGAAA GAAGGTGAAC TTGGCAGAGC TGTTC AAGGA CAAGAAAGGT 240
186
187 GTTTTGT TTTG GAGTCCCTGG GGCATTTACA CCTGGCTGTT CCAAGACCCA TCTGCCTGGG 300
188
189 TTTGTGGAGC AAGCCGGAGC TCYGAAGGCC AAGGGAGCAC AAGTGGTGGC CTGTCTGAGT 360
190
191 GTTAATGATG YCTTCGTGAC TGCAGAGTGG GGTGAGCCC ACCAGGCAGA AGGCAAGGTT 420
192
193 CAGCTCCTGG CTGACCCAC TGGAGCTTTT GGAAAGGAGA CAGATTTACT ACTAGATGAT 480
194
195 TCTTTGGTGT CTCTCTTTGG GAATCGTCGG CTAAAAAGGT TCTCCATGGT GATAGACAAG 540
196
197 GCGGTAGTAA AGGCACTGAA CGTGGAGCCG GATGGCACAG GCCTCACCTG CAGCCTGGCC 600
198
199 CCCAACATCC TCTCACA ACT CTGAGGCCCT GACCAGAATG TCCTCTGACT CTCCCATCTC 660
200
201 CTCCACCCAG CTCTGGGCCA AAGGCCAGT ACCTCCTTAC CTGAGGGCCA CTGGAATGGA 720
202
203 ACCTTGACAA TATTTCTGCA ATAAACAGTT TAATTTGTGA AAAAAAAAAA AAAAAAAAAA 780
204
205

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/486,167DATE: 10/03/2000
TIME: 22:46:47

INPUT SET: S35961.raw

206 (2) INFORMATION FOR SEQ ID NO: 4:
207
208 (i) SEQUENCE CHARACTERISTICS:
209 (A) LENGTH: 162 amino acids
210 (B) TYPE: amino acid
211 (C) STRANDEDNESS: single
212 (D) TOPOLOGY: linear
213
214 (ii) MOLECULE TYPE: peptide
215
216 (iii) HYPOTHETICAL: NO
217
218 (iv) ANTI-SENSE: NO
219
220 (vi) ORIGINAL SOURCE:
221 (A) ORGANISM: Rattus Rattus
222
223 (ix) FEATURE:
224 (A) NAME/KEY: Modified-site
225 (B) LOCATION:17
226 (D) OTHER INFORMATION:/product= "Glu or Gly"
227
228 (ix) FEATURE:
229 (A) NAME/KEY: Modified-site
230 (B) LOCATION:63
231 (D) OTHER INFORMATION:/product= "Leu or Pro"
232
233 (ix) FEATURE:
234 (A) NAME/KEY: Modified-site
235 (B) LOCATION:79
236 (D) OTHER INFORMATION:/product= "Ala or Val"
237
238
239 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
240
241 Met Ala Pro Ile Lys Val Gly Asp Thr Ile Pro Ser Val Glu Val Phe
242 1 5 10 15
243
244 Xaa Gly Glu Pro Gly Lys Lys Val Asn Leu Ala Glu Leu Phe Lys Asp
245 20 25 30
246
247 Lys Lys Gly Val Leu Phe Gly Val Pro Gly Ala Phe Thr Pro Gly Cys
248 35 40 45
249
250 Ser Lys Thr His Leu Pro Gly Phe Val Glu Gln Ala Gly Ala Xaa Lys
251 50 55 60
252
253 Ala Lys Gly Ala Gln Val Val Ala Cys Leu Ser Val Asn Asp Xaa Phe
254 65 70 75 80
255
256 Val Thr Ala Glu Trp Gly Arg Ala His Gln Ala Glu Gly Lys Val Gln
257 85 90 95
258

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/486,167DATE: 10/03/2000
TIME: 22:46:48**INPUT SET: S35961.raw**

Line	Error	Original Text
5	Mandatory Value Not Present	(i) APPLICANT:
6	Unknown or Misplaced Identifier	(A) NAME: UNIVERSITE CATHOLIQUE DE LOUVAIN
8	Unknown or Misplaced Identifier	(B) STREET: Place de l' Universite, 1
9	Unknown or Misplaced Identifier	(C) CITY: LOUVAIN-LA-NEUVE
10	Unknown or Misplaced Identifier	(E) COUNTRY: BELGIUM
11	Unknown or Misplaced Identifier	(F) POSTAL CODE (ZIP): B-1348
13	Unknown or Misplaced Identifier	(A) NAME: UNIVERSITE DE MONS-HAINAUT
14	Unknown or Misplaced Identifier	(B) STREET: Place du Parc 20
15	Unknown or Misplaced Identifier	(C) CITY: MONS
16	Unknown or Misplaced Identifier	(E) COUNTRY: BELGIUM
17	Unknown or Misplaced Identifier	(F) POSTAL CODE (ZIP): B-7000
155	Stop Codon at end of sequence removed - no error	(2) INFORMATION FOR SEQ ID NO: 3:

PAGE: 1

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION *US/09/486,167*

DATE: 10/03/2000
TIME: 22:46:48

INPUT SET: S35961.raw

ADDRESSEE
STREET
CITY
STATE
COUNTRY
ZIP
CORRESPONDENCE ADDRESS
APPLICATION NUMBER
FILING DATE
CLASSIFICATION
CURRENT APPLICATION DATA
APPLICATION NUMBER
FILING DATE
PRIOR APPLICATION DATA